



SEQUENCE LISTING

<110> ADLER, JON ELLIOT

<120> T2R TASTE RECEPTORS AND GENES ENCODING SAME

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<141> 2001-04-05

<150> 60/195,532

<151> 2000-04-07

<150> 60/247,014

<151> 2000-11-13

<160> 31

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 2

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 35 40 45

Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
 50 55 60

Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
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Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
 85 90 95

Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
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Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
 115 120 125

Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
 130 135 140

Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
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Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
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Asn Asn Asn Thr Arg Leu Asn Trp Gln Ile Lys Asp Leu Asn Leu Phe
 180 185 190

Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
 195 200 205

Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
 210 215 220

Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
 225 230 235 240

Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
 245 250 255

Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
 260 265 270

Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
 275 280 285

Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
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<210> 3
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35 40 45
Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
50 55 60
Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
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Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
85 90 95
Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
100 105 110
Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
115 120 125
Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
130 135 140

Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
 145 150 155 160
 Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
 165 170 175
 Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
 180 185 190
 Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
 195 200 205
 Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
 210 215 220
 Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
 225 230 235 240
 Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
 245 250 255
 Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
 260 265 270
 Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
 275 280 285
 Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
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 Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
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 <212> DNA
 <213> Homo sapiens

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 35 40 45
 Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
 50 55 60
 Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
 65 70 75 80
 Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
 85 90 95
 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
 100 105 110
 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
 115 120 125
 Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
 130 135 140
 Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu
 145 150 155 160
 Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
 165 170 175
 Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
 180 185 190
 Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
 195 200 205
 Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
 210 215 220
 Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
 225 230 235 240
 Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
 245 250 255

Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
 260 265 270

Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
 275 280 285

Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
 290 295 300

Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
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Gln Thr Leu

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Asn Ser Val Glu Val
 65 70 75 80

Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
 85 90 95

Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125

Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
 130 135 140

Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Asn
 165 170 175

Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190

Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255

Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270

Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

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Lys Thr Ser Ser Pro
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 <212> DNA
 <213> Homo sapiens

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 atctcctcag ctgatcaa at tattgctgct ctggcagtct ccagagttgg tttgctctgg 180

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<210> 10
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<213> Homo sapiens

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      20          25          30

Ile Ala Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile
      35          40          45

Ala Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
      50          55          60

His Trp Tyr Ser Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val
      65          70          75          80

Ile Ile Phe Ile Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
      85          90          95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
      100         105         110

Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
      115         120         125

Val Leu Val Ile Val Leu Gly Ser Leu Phe Phe Leu Val Cys His Leu
      130         135         140

Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Glu Glu Cys His Glu Gly
      145         150         155         160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Met His Leu Ser Asn
      165         170         175

Leu Thr Val Ala Met Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
      180         185         190

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Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Ile His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Ile Leu Leu Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Leu Ile Ile Ser Phe Trp Asn Phe Lys Met Arg Pro
 245 250 255

Lys Glu Ile Val Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro
 260 265 270

Ser Phe His Ser Phe Ile Leu Ile Trp Gly Asn Lys Thr Leu Lys Gln
 275 280 285

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Asn Gln Ser Thr Pro
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<212> DNA

<213> Homo sapiens

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<212> PRT

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 35 40 45

 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60

 Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
 65 70 75 80

 Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
 85 90 95

 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125

 Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
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 Phe Val Ile Asn Met Lys Glu Ile Val Arg Thr Lys Glu Tyr Glu Gly
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 Asn Leu Thr Trp Lys Ile Lys Leu Arg Ser Ala Val Tyr Leu Ser Asp
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 Ala Thr Val Thr Thr Leu Gly Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190

 Leu Cys Phe Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

 Ile Lys Ala Leu Gln Thr Val Ile Phe Phe Leu Leu Leu Cys Ala Val
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 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255

 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
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 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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 Lys Pro Ser Ser Pro
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35 40 45
Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe
50 55 60
Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val
65 70 75 80
Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met
85 90 95
Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn
100 105 110
Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val
115 120 125
Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
130 135 140
Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175
 Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190
 Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240
 Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln
 245 250 255
 Ser Lys Leu Val Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro
 260 265 270
 Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Leu Trp Gln Met Thr Arg
 290 295

<210> 15
 <211> 900
 <212> DNA
 <213> Homo sapiens

<400> 15
 atgataaac ttctatacat tttttttca attctaataa tggtttatt tggtctcgga 60
 aactttgcc aatggcttcat agcactggta aatttcattt actgggtgaa gagaaaaaaag 120
 atctccctcag ctgaccaaattt tctcactgct ctggcggtct ccagaatttg tttgctctgg 180
 gcattattat taaaattggta tttaactgtg ttgaatccag ctttttatag tgtagaatta 240
 agaattactt cttataatgc ctgggttgc accaaccatt tcagcatgtg gcttgctgct 300
 aacctcagca tattttattt gctcaagattt gccaatttctt ccaaccttctt ttttcttcatt 360
 ttaaaggagga gagtttaggag tgcattctg gtgatactgt tggggactttt gatatttttg 420
 gtttgcattc ttcttgcgc aaacatggat gagagtatgt gggcagaaga atatgaagga 480
 aacatgactg ggaagatgaa attgaggaat acagtagatc tttcatattt gactgtaact 540
 accctatggaa gcttcataacc cttaactctg tccctgatat cttttctgat gctaatttgt 600
 tctctgtgtt aacatctcaa gaagatgcag ctccatggag aaggatcgca agatctcagc 660
 accaagggtcc acataaaaagc tttgcaaact ctgatctcct tcctcttgcattt atgtgccatt 720
 ttctttctat tcctaattcgt ttgggttgg agtccttagga ggctgcccggaa tgaccgggtt 780
 gtcatggta gcaaggctgt tggaaacata tatcttgcatt tcgactcatt catcctaattt 840
 tggagaacca agaagctaaa acacacctttt cttttgattt tgcgtcagat taggtgctga 900

<210> 16
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ile Thr Phe Leu Tyr Ile Phe Phe Ser Ile Leu Ile Met Val Leu
 1 5 10 15

 Phe Val Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Phe
 20 25 30

 Ile Asp Trp Val Lys Arg Lys Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45

 Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu
 50 55 60

 Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
 65 70 75 80

 Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met
 85 90 95

 Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

 Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val
 115 120 125

 Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu
 130 135 140

 Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly
 145 150 155 160

 Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr
 165 170 175

 Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu
 180 185 190

 Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

 Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
 210 215 220

 Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

 Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
 245 250 255

 Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
 260 265 270

 Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
 275 280 285

 Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
 290 295

<210> 17
<211> 924
<212> DNA
<213> Homo sapiens

<400> 17
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attgcagcga atggcttcat tgtgctggtg ctgggcagg agtggctgcg atatggcagg 120
ttgctgcctt tggatatgtat cctcatttgc ttgggtgcct cccgcttctg cctgcagttg 180
gttgggacgg tgcacaactt ctactactct gcccagaagg tcgagtaactc tgggggtctc 240
ggccgacagt tctccatct acactggcac ttctctaact cagccacctt ctgggttgc 300
agctggctca gtgtcctgtt ctgtgtgaag attgctaaca tcacacactc caccttcctg 360
tggctgaagt ggagggttccc agggtgggtg ccctggctcc tgggggtctc tgcctgatc 420
tccttcataca taaccctgtt gttttttgg gtgaactacc ctgtatataca agaattttta 480
attagaaaat ttcttggaa catgacctac aagtggaaata caaggataga aacatactat 540
ttcccatccc tgaaactggt catctggtca attcctttt ctgttttct ggtctcaatt 600
atgctgttaa ttaattctt gaggaggcat actcagagaa tgcagcacaa cgggcacagc 660
ctgcaggacc ccagcaccca ggctcacacc agagctctga agtccctcat ctccttcctc 720
attcttatg ctctgtcctt tctgtccctg atcattgatg ccgcaaaatt tatctccatg 780
cagaacgact ttactggcc atggcaaatt gcagtctacc tgcataatc tgcctatccc 840
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gcaaggggct tctgggtggc cttag 924

<210> 18
<211> 307
<212> PRT
<213> Homo sapiens

<400> 18
Met Gln Ala Ala Leu Thr Ala Phe Phe Val Leu Leu Phe Ser Leu Leu
1 5 10 15
Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
20 25 30
Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
35 40 45
Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
50 55 60
His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
65 70 75 80
Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
85 90 95
Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile Ala
100 105 110
Asn Ile Thr His Ser Thr Phe Leu Trp Leu Lys Trp Arg Phe Pro Gly
115 120 125
Trp Val Pro Trp Leu Leu Leu Gly Ser Val Leu Ile Ser Phe Ile Ile
130 135 140

Thr Leu Leu Phe Phe Trp Val Asn Tyr Pro Val Tyr Gln Glu Phe Leu
 145 150 155 160
 Ile Arg Lys Phe Ser Gly Asn Met Thr Tyr Lys Trp Asn Thr Arg Ile
 165 170 175
 Glu Thr Tyr Tyr Phe Pro Ser Leu Lys Leu Val Ile Trp Ser Ile Pro
 180 185 190
 Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
 195 200 205
 Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
 210 215 220
 Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
 225 230 235 240
 Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
 245 250 255
 Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
 260 265 270
 Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
 275 280 285
 Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe
 290 295 300
 Trp Val Ala
 305

<210> 19
 <211> 930
 <212> DNA
 <213> Homo sapiens

<400> 19
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 aattttgcta atggcttcat agcattggta aattccattt agtgggtcaa gagacaaaag 120
 atctcttttgc ctgaccataat tctcaactgct ctggcagtct ccagagttgg tttactctgg 180
 gtatttagtat taaattggta tgcaactgag ttgaatccag ctttaacag tatagaagta 240
 agaattactg cttacaatgt ctgggcagta atcaaccatt tcagcaactg gcttgctact 300
 agcctcagca tattttatgt gctcaagatt gccaattttct ccaaccttat ttttcttcac 360
 ttaaagagga gagttaaagag tggttgttctg gtgataactat tggggcctt gctattttg 420
 gtttgtcatc ttttgtat aaacatgaat cagattatat ggacaaaaga atatgaagga 480
 aacatgactt ggaagatcaa actgaggagt gcaatgtacc tttcaaatac aacggtaacc 540
 atccttagcaa acttagttcc cttcaactctg accctgatat cttttctgct gttaatctgt 600
 tctctgttca aacatctcaa aaagatgcag ctccatggca aaggatctca agatcccagc 660
 atgaagggcc acataaaaagc tttgcaaact gtgacccctt tcctcttgat atgtgccatt 720
 tactttctgt ccataatcat gtcagttgg agttttgaga gtctggaaaa caaacctgtc 780
 ttcatgttct gcgaagctat tgcattcagc tattcattcaa cccaccctt catcctgatt 840
 tggggaaaca agaagctaaa gcagactttt ctttcagttt tggatgtt gaggtactgg 900
 gtgaaaggag agaaggccatc atcttcatag 930

<210> 20
<211> 309
<212> PRT
<213> Homo sapiens

<400> 20
Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
1 5 10 15
Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20 25 30
Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
35 40 45
Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Val Leu
50 55 60
Asn Trp Tyr Ala Thr Glu Leu Asn Pro Ala Phe Asn Ser Ile Glu Val
65 70 75 80
Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Ile Asn His Phe Ser Asn
85 90 95
Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110
Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
115 120 125
Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
130 135 140
Phe Val Ile Asn Met Asn Gln Ile Ile Trp Thr Lys Glu Tyr Glu Gly
145 150 155 160
Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr Leu Ser Asn
165 170 175
Thr Thr Val Thr Ile Leu Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
180 185 190
Ile Ser Phe Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205
Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Met Lys Val His
210 215 220
Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
225 230 235 240
Tyr Phe Leu Ser Ile Ile Met Ser Val Trp Ser Phe Glu Ser Leu Glu
245 250 255
Asn Lys Pro Val Phe Met Phe Cys Glu Ala Ile Ala Phe Ser Tyr Pro
260 265 270

Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp His Val Arg Tyr Trp Val Lys Gly Glu
 290 295 300

Lys Pro Ser Ser Ser
 305

<210> 21
<211> 930
<212> DNA
<213> Homo sapiens

<400> 21
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atctcctcag ctgaccataat cctcactgct ctgggtgtt ccagaattgg tttactctgg 180
gtcatattat tacattggta tgcaaattgtt tttatttcag ctttatataag ttcagaagta 240
ggagctgttg cttctaataat ctcagcaata atcaaccatt tcagcatctg gcttgcgtct 300
agcctcagca tattttattt gctcaagatt gccaattttt ccaaccttat tttctccac 360
ctaaagaaga gaatttaggag tggtgttctg gtgatactgt tgggtccctt ggtatTTTg 420
atttgttaatc ttgctgttat aaccatggat gacagtgtgt ggacaaaaga atatgaagga 480
aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaaactt gactgtaagc 540
acactagcaa acctcatacc ctccattctg accctataat ttttgcgtct gttaatctgt 600
tctctgcata aacatctcaa gaagatgcag ctccatggca aaggatctca agatctcagc 660
accaaggc acataaaaagc tttgcaaact gtgatctctt tcctcatgtt atatgccatt 720
tactttctgt atctaataatcattt aatctttgg aatctttgaa cacagcagaa caaacttgta 780
ttcctgcattt gccaaactctt tggaatcatg tatccttcat tccactcatt ttcctgatt 840
atgggaagca gggaaactaaa acagacgttt ctttcagttt tatgtcaggt cacatgctt 900
gtgaaaggac agcaaccctc aactccatag 930

<210> 22
<211> 885
<212> DNA
<213> Homo sapiens

<400> 22
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atctcatcag ctgaccataat ttctcactgct tctgggtgtt tccagagttt gtttactctg 180
ggtcatattat ttacattggat atgcaactgtt gtttattttt gtttccatata gattagaagt 240
aagaattttt ggttctaataat ctcagcaata accaagcat ttcagcatct ggggtttact 300
agcctcagca tattttattt gctcaagactt gccaattttt ccaaccttat ttttctccac 360
ctaaagaaaa ggattaagaa tggtgttgtt gtgatgtgtt tggggccctt ggtatTTTc 420
atttgttaatc ttgctctgtat aaccacgggt gagagtgtgtt ggacaaaaga atatgaagga 480
aatttgcattt ggatgatcaa attgaggaat gcaatacacc tttcaaactt gactgtaacc 540
atgccagcaa acgtcacacc ctgcactctg acactataat ttttgcgtct gttaatcttat 600
tctccatgtt aacatgtcaa gaagatgcag ctccatggca aaggatctca acatctcagc 660
accaaggc acataaaaagc tttgcaaact gtgatctctt tccttatgtt atttgccatt 720
tactttctgtt gtctaataatcattt aatctttgg aatctttgaa ctcagcagag caaacttgta 780
ttcctgcattt accaaactctt tggttcatg tatctttgtt tccactcatt catcctgact 840
atgggaagta ggaagccaaa acagaccttt ctttcagttt tgtga 885

<210> 23
<211> 912
<212> DNA
<213> Mus sp.

<400> 23
atgacccccc cttcccaagc tatttatcac atggcatca tgacacgaga gtttctcatc 60
gggactacag tgaatggatt ctttatcatt gtgaactgct atgacttgtt caagagccga 120
acgttcctga tcctgcagac cctcttgatg tgcacaggc tgcacaggact cggctctgcag 180
ataatgccta tgacccaaag cttcttcttgc gtgttcttc catactctta tgaggaaaat 240
atttatagtt cagatataat gttcgctctgg atgttcttca gtcgattgg cctctgggtt 300
gccacatgtc tctctgtctt ttactgcctc aagatttcag gtttactcc accctgggtt 360
cttggctga aattcagaat ttcaaagctc atatttggc tgcttctggc cagcttgcgtg 420
gcctctctgg gcactgcaac tgcgtgcattc gagtaggtt tcccttaat tgaggatggc 480
tatgtcctga gaaacgcagg actaaatgtt agtaatgcca agctagttagt aaataatgac 540
ttgcctctca tcaacctgtat cctcctgtctt cccctgtctg tgtttgcgtat gtgcacccct 600
atgttatttg tttctcttta caagcacatg cactggatgc aaagcgaatc tcacaagctg 660
tcaagtgcctca gaaccgaagc tcatataat gcattaaaga cagtgacaac attctttgtt 720
ttctttgttt ctactttgc tgccttcattt gcaaatatgaa catttagaat tccatacaga 780
agtcatcagt tctcgctgtt gaaggaaatc atggcagcat atccccccgg ccactctgtc 840
ataatgcctca tgtagtaactc taagttcaaa gacttattca ggagaatgtat ctgtctacag 900
aaggaagagt ga 912

<210> 24
<211> 303
<212> PRT
<213> Mus sp.

<400> 24
Met Thr Ser Pro Phe Pro Ala Ile Tyr His Met Val Ile Met Thr Ala
1 5 10 15
Glu Phe Leu Ile Gly Thr Thr Val Asn Gly Phe Leu Ile Ile Val Asn
20 25 30
Cys Tyr Asp Leu Phe Lys Ser Arg Thr Phe Leu Ile Leu Gln Thr Leu
35 40 45
Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met
50 55 60
Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn
65 70 75 80
Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile
85 90 95
Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
100 105 110
Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser
115 120 125
Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly
130 135 140

Thr Ala Thr Val Cys Ile Glu Val Gly Pro Leu Ile Glu Asp Gly
 145 150 155 160

Tyr Val Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val
 165 170 175

Arg Asn Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Pro Leu
 180 185 190

Ser Val Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys
 195 200 205

His Met His Trp Met Gln Ser Glu Ser His Lys Leu Ser Ser Ala Arg
 210 215 220

Thr Glu Ala His Ile Asn Ala Leu Lys Thr Val Thr Thr Phe Phe Cys
 225 230 235 240

Phe Phe Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg
 245 250 255

Ile Pro Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala
 260 265 270

Ala Tyr Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys
 275 280 285

Phe Lys Asp Leu Phe Arg Arg Met Ile Cys Leu Gln Lys Glu Glu
 290 295 300

<210> 25
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> MOD_RES
 <222> (2)
 <223> Phe or Gly

<220>
 <221> MOD_RES
 <222> (3)
 <223> Ile, Val or Leu

<220>
 <221> MOD_RES
 <222> (4)
 <223> Val or Leu

<220>
 <221> MOD_RES
 <222> (6)
 <223> Ile or Val

<220>
 <221> MOD_RES

<222> (7)
<223> Leu or Val

<220>
<221> MOD_RES
<222> (10)
<223> Gly or Thr

<220>
<221> MOD_RES
<222> (13)
<223> Val or Ala

<220>
<221> MOD_RES
<222> (18)
<223> Ile or Met

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 25
Glu Xaa Xaa Xaa Gly Xaa Xaa Gly Asn Xaa Phe Ile Xaa Leu Val Asn
1 5 10 15

Cys Xaa Asp Trp
20

<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (1)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (2)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (3)
<223> Ile or Leu

<220>
<221> MOD_RES
<222> (5)
<223> Thr or Ile

<220>
<221> MOD_RES

<222> (6)
<223> Gly, Ala or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Cys, Gly or Phe

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 26
Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu
1 5 10

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (3)
<223> Leu or Phe

<220>
<221> MOD_RES
<222> (4)
<223> Ser, Thr or Asn

<220>
<221> MOD_RES
<222> (5)
<223> Leu, Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (8)
<223> Ala or Thr

<220>
<221> MOD_RES
<222> (10)
<223> Cys, Ser or Asn

<220>
<221> MOD_RES
<222> (12)
<223> Ser, Asn or Gly

<220>
<221> MOD_RES
<222> (13)
<223> Ile or Val

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 27
Asn His Xaa Xaa Xaa Trp Xaa Xaa Thr Xaa Leu Xaa Xaa
1 5 10

<210> 28
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (3)
<223> Phe or Cys

<220>
<221> MOD_RES
<222> (8)
<223> Asn or Ser

<220>
<221> MOD_RES
<222> (11)
<223> His or Asn

<220>
<221> MOD_RES
<222> (12)
<223> Pro or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Leu, Ile or Val

<220>
<221> MOD_RES
<222> (16)
<223> Trp or Tyr

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 28
Phe Tyr Xaa Leu Lys Ile Ala Xaa Phe Ser Xaa Xaa Xaa Phe Leu Xaa
1 5 10 15

Leu Lys

<210> 29
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (4)
<223> Ile, Phe or Val

<220>
<221> MOD_RES
<222> (8)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (10)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (11)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (12)
<223> Gln or Lys

<220>
<221> MOD_RES
<222> (13)
<223> Met or Ile

<220>
<221> MOD_RES
<222> (14)
<223> Gln or Lys

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 29
Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa
1 5 10

<210> 30
<211> 14
<212> PRT
<213> Artificial Sequence

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<220>
<221> MOD_RES
<222> (3)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (8)
<223> Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (10)
<223> Pro, Ser or Asn

<220>
<221> MOD_RES
<222> (13)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (14)
<223> Gln or Arg

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<400> 30
His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa
     1           5           10

<210> 31
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide translocation domain

<400> 31
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     1           5           10           15

Thr Gly Val Val
     20
```